

AS AP
2-22-02



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,826

DATE: 05/21/2002

TIME: 15:40:34

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3 <110> APPLICANT: Davis, Peter D
 5 <120> TITLE OF INVENTION: Chimeric proteins mediating targeted apoptosis
 7 <130> FILE REFERENCE: 620-179
 9 <140> CURRENT APPLICATION NUMBER: US 10/018,826
 C--> 10 <141> CURRENT FILING DATE: 2002-04-22
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02449
 13 <151> PRIOR FILING DATE: 2000-06-26
 15 <150> PRIOR APPLICATION NUMBER: GB 9914650.8
 16 <151> PRIOR FILING DATE: 1999-06-24
 18 <160> NUMBER OF SEQ ID NOS: 22
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 84
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Homo sapiens
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 29 1 5 10 15
 31 Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile
 32 20 25 30
 34 Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu
 35 35 40 45
 37 Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu
 38 50 55 60
 40 Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
 41 65 70 75 80
 43 Gln Thr Ile Ile
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 48 <211> LENGTH: 86
 49 <212> TYPE: PRT
 50 <213> ORGANISM: Homo sapiens
 52 <400> SEQUENCE: 2
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 54 1 5 10 15
 56 Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile Asp Arg
 57 20 25 30
 59 Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr Ser Met
 60 35 40 45
 62 Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr Leu Glu
 63 50 55 60
 65 Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys Leu Glu
 66 65 70 75 80
 68 Asp Ile Glu Glu Ala Leu

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74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
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78 <221> NAME/KEY: CDS
79 <222> LOCATION: (116)..(1411)
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
83     construct encoding a chimeric protein containing
84     the extracellular domain of CD44H and the
85     transmembrane and cytoplasmic domains of human Fas
87 <400> SEQUENCE: 3
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89 cgcccaggga tcctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg 118
90                                     Met
91                                     1
92 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
93 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
94                                     5          10          15
95 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
96 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
97                                     20          25          30
98 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
99 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
100                                     35          40          45
101 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
102 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
103                                     50          55          60          65
104 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
105 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
106                                     70          75          80
107 ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406
108 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
109                                     85          90          95
110 gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454
111 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
112                                     100         105         110
113 tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502
114 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
115                                     115         120         125
116 aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550
117 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile
118                                     130         135         140         145
119 act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac 598
120 Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr
121                                     150         155         160
122 aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac 646

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135	Arg	Thr	Asn	Pro	Glu	Asp	Ile	Tyr	Pro	Ser	Asn	Pro	Thr	Asp	Asp	Asp	
136				165					170					175			
138	gtg	agc	agc	ggc	tcc	tcc	agt	gaa	agg	agc	agc	act	tca	gga	ggg	tac	694
139	Val	Ser	Ser	Gly	Ser	Ser	Ser	Glu	Arg	Ser	Ser	Thr	Ser	Gly	Gly	Tyr	
140			180					185					190				
142	atc	ttt	tac	acc	ttt	tct	act	gta	cac	ccc	atc	cca	gac	gaa	gac	agt	742
143	Ile	Phe	Tyr	Thr	Phe	Ser	Thr	Val	His	Pro	Ile	Pro	Asp	Glu	Asp	Ser	
144		195					200					205					
146	ccc	tgg	atc	acc	gac	agc	aca	gac	aga	atc	cct	gct	acc	aga	gac	caa	790
147	Pro	Trp	Ile	Thr	Asp	Ser	Thr	Asp	Arg	Ile	Pro	Ala	Thr	Arg	Asp	Gln	
148	210					215					220					225	
150	gac	aca	ttc	cac	ccc	agt	ggg	ggg	tcc	cat	acc	act	cat	gga	tct	gaa	838
151	Asp	Thr	Phe	His	Pro	Ser	Gly	Gly	Ser	His	Thr	Thr	His	Gly	Ser	Glu	
152				230						235				240			
154	tca	gat	gga	cac	tca	cat	ggg	agt	caa	gaa	ggg	gga	gca	aac	aca	acc	886
155	Ser	Asp	Gly	His	Ser	His	Gly	Ser	Gln	Glu	Gly	Gly	Ala	Asn	Thr	Thr	
156			245						250					255			
158	tct	ggg	cct	ata	agg	aca	ccc	caa	att	cca	gaa	tgg	ctg	atc	atc	ctt	934
159	Ser	Gly	Pro	Ile	Arg	Thr	Pro	Gln	Ile	Pro	Glu	Trp	Leu	Ile	Ile	Leu	
160		260					265						270				
162	tgt	ctt	ctt	ctt	ttg	cca	att	cca	cta	att	gtt	tgg	gtg	aag	aga	aag	982
163	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg	Lys	
164		275				280						285					
166	gaa	gta	cag	aaa	aca	tgc	aga	aag	cac	aga	aag	gaa	aac	caa	ggg	tct	1030
167	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly	Ser	
168	290					295					300					305	
170	cat	gaa	tct	cca	acc	tta	aat	cct	gaa	aca	gtg	gca	ata	aat	tta	tct	1078
171	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu	Ser	
172				310						315				320			
174	gat	gtt	gac	ttg	agt	aaa	tat	atc	acc	act	att	gct	gga	gtc	atg	aca	1126
175	Asp	Val	Asp	Leu	Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met	Thr	
176			325						330					335			
178	cta	agt	caa	gtt	aaa	ggc	ttt	gtt	cga	aag	aat	ggg	gtc	aat	gaa	gcc	1174
179	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu	Ala	
180		340					345					350					
182	aaa	ata	gat	gag	atc	aag	aat	gac	aat	gtc	caa	gac	aca	gca	gaa	cag	1222
183	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu	Gln	
184		355				360						365					
186	aaa	gtt	caa	ctg	ctt	cgt	aat	tgg	cat	caa	ctt	cat	gga	aag	aaa	gaa	1270
187	Lys	Val	Gln	Leu	Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys	Glu	
188	370					375					380					385	
190	gcg	tat	gac	aca	ttg	att	aaa	gat	ctc	aaa	aaa	gcc	aat	ctt	tgt	act	1318
191	Ala	Tyr	Asp	Thr	Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	Thr	
192				390						395				400			
194	ctt	gca	ggg	aaa	att	cag	act	atc	atc	ctc	aag	gac	att	act	agt	gac	1366
195	Leu	Ala	Gly	Lys	Ile	Gln	Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser	Asp	
196			405						410					415			
198	tca	gaa	aat	tca	aac	ttc	aga	aat	gaa	atc	caa	agc	ttg	gtc	tag		1411
199	Ser	Glu	Asn	Ser	Asn	Phe	Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val			

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207 <212> TYPE: PRT
208 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric protein
212     containing the extracellular domain of CD44H and the
213     transmembrane and cytoplasmic domains of human Fas
215 <400> SEQUENCE: 4
216 Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
217   1          5          10          15
218 Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
219          20          25          30
220 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
221          35          40          45
222 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
223          50          55          60
224 Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
225   65          70          75          80
226 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
227          85          90          95
228 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
229          100         105         110
230 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
231          115         120         125
232 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
233          130         135         140
234 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
235  145         150         155         160
236 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
237          165         170         175
238 Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
239          180         185         190
240 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
241          195         200         205
242 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
243          210         215         220
244 Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser
245  225         230         235         240
246 Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
247          245         250         255
248 Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
249          260         265         270
250 Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
251          275         280         285
252 Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
253          290         295         300

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254 Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu
255 305                      310                      315                      320
256 Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met
257                      325                      330                      335
258 Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu
259                      340                      345                      350
260 Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu
261                      355                      360                      365
262 Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys
263                      370                      375                      380
264 Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys
265 385                      390                      395                      400
266 Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser
267                      405                      410                      415
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269                      420                      425                      430
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274 <211> LENGTH: 1483
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <221> NAME/KEY: CDS
280 <222> LOCATION: (116)..(1426)
282 <220> FEATURE:
283 <223> OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid
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285     the extracellular and transmembrane domains of CD44H
286     and the cytoplasmic domain of human Fas
288 <400> SEQUENCE: 5
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291 cgcccaggga tcctccagct cctttcgccc gcgccctccg ttcgctccgg acacc atg 118
292                                     Met
293                                     1
295 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
296 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
297                      5                      10                      15
299 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
300 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
301                      20                      25                      30
303 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
304 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
305                      35                      40                      45
307 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
308 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
309 50                      55                      60                      65
311 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
312 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
313                      70                      75                      80
315 ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406

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VERIFICATION SUMMARY

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